

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1	((mitochondrial near3 respiratory) same (\$5array or \$4chip)) and @ad<"20020321"	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/11/24 11:04
L2	165	((mitochondrial) same (\$5array or \$4chip)) and @ad<"20020321"	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/11/24 11:04



Sequence Revision History

[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Book](#)

Find (Accessions, GI numbers or Fasta style SeqIds)



About Entrez

Show difference in



format

Entrez

Gi	Version	Update Date
565648	1	Aug 1 2006 12:46 PM
565648	1	Nov 9 1994 10:44 AM

Search for Genes

Entrez Gene provides gene-specific data for multiple taxa

Query= gi|565648|dbj|D26599.1|HUMPSH2 Homo sapiens mRNA for proteasome subunit HsC7-I, complete cds (762 letters)

Help|FAQ

Batch Entrez: Upload a file of GI or accession numbers to retrieve protein or nucleotide sequences

<gi|565648|dbj|D26599|HUMPSH2 Human mRNA for proteasome subunit HsC7-I
Length = 762

Score = 1421 bits (717), Expect = 0.0
Identities = 747/762 (98%)
Strand = Plus / Plus

Check sequence revision history

How to create WWW links to Entrez

LinkOut

My NCBI (Cubby)

Related resources

BLAST

Reference sequence project

Entrez Gene

Clusters of orthologous groups

Protein reviews on the web

```

Query: 1   cggacctgcagccctggccttcgccaccatggagtagctcatcggtatccaaggcccg 6
          |||
Sbjct: 1   cggacctgcagccctggccttcgccaccatggagtagctcatcggtatccaaggcccg 6

Query: 61  actatgttcttgtcgctccgaccgggtggccgagcaatattgtccagatgaaggacg 1
          |||
Sbjct: 61  actatgttcttgtcgctccgaccgggtggccgagcaatattgtccagatgaaggacg 1

Query: 121 atcatgacaagatgtttaagatgagtgaagagatattactcctgtgtgtggagaggctg 1
          |||
Sbjct: 121 atcatgacaagatgtttaagatgagtgaagagatattactcctgtgtgtggagaggctg 1

Query: 181 gagacactgtacagtttgcagaatatattcagaaaaacgtgcaactttataagatgcgaa 2
          |||
Sbjct: 181 gagacactgtacagtttgcagaatatattcagaaaaacgtgcaactttataagatgcgaa 2

Query: 241 atggatatgaattgtctccacggcagcagctaacttcacacgccgaaacctgggtgact 3
          |||
Sbjct: 241 atggatatgaattgtctccacggcagcagctaacttcacacgccgaaacctgggtgact 3

Query: 301 gtcttcggagtcggaccccatatcatgtgaacctcctcctgggtggctatgatgagcatg 3
          |||
Sbjct: 301 gtcttcggagtcggaccccatatcatgtgaacctcctcctgggtggctatgatgagcatg 3

Query: 361 aagggccagcgtgtattacatggactacctggcagccttgccaaggcccttttgcag 4
          |||
Sbjct: 361 aagggccagcgtgtattacatggactacctggcagccttgccaaggcccttttgcag 4
    
```

```

Query:   421  cccacggctatgggtgccttccctgactctcagtatcctcgaccgatactacacaccgacta 4
          |||
Sbjct:   421  cccacggctatgggtgccttccctgactctcagtatcctcgaccgatactacacaccgacta 4

Query:   481  tctcacgtgagagggcagtggaactccttaggaaatgtctggaggagctccagaaacgct 5
          |||
Sbjct:   481  tctcacgtgagagggcagtggaactccttaggaaatgtctggaggagctccagaaacgct 5

Query:   541  tcatcctgaatctgccaaccttcagtgttcgaatcattgacaaaaatggcatccatgacc 6
          |||
Sbjct:   541  tcatcctgaatctgccaaccttcagtgttcgaatcattgacaaaaatggcatccatgacc 6

Query:   601  tggataacatttcttccccaacagggtcctaacatcatgtcctccctcccaacttggc 6
          |||
Sbjct:   601  tggataacatttcttccccaacagggtcctaacatcatgtcctccctcccaacttggc 6

Query:   661  agggaacnnnnnnngatgggctcctttannnnnnnctactcttttcaggcgcaactcttg 7
          |||
Sbjct:   661  agggaacttttttttgatgggctcctttattttttctactcttttcaggcgcaactcttg 7

Query:   721  ataaatggttaattcagaataaagggtgactatggatataatt 762
          |||
Sbjct:   721  ataaatggttaattcagaataaagggtgactatggatataatt 762

```

Score = 28.2 bits (14), Expect = 0.002
Identities = 14/14 (100%)
Strand = Plus / Minus

```
Query: 396 gccttggccaaggc 409
      |||||
Sbjct: 409 gccttggccaaggc 396
```

Score = 24.3 bits (12), Expect = 0.028
Identities = 12/12 (100%)
Strand = Plus / Minus

```
Query: 481 tctcacgtgaga 492
      |||||
Sbjct: 492 tctcacgtgaga 481
```

Lambda	K	H
1.37	0.711	1.31

Gapped		
Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 191
Number of extensions: 5
Number of successful extensions: 5
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 5
Number of HSP's successfully gapped: 4
Length of query: 762
Length of database: 762
Length adjustment: 9
Effective length of query: 753
Effective length of database: 753
Effective search space: 567009
Effective search space used: 567009
X1: 8 (15.9 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 8 (16.4 bits)
S2: 8 (16.4 bits)

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